RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10	Sa	0	76	<u>8</u>
Source:		P	$\mathcal{T}_{\vec{+}}$		
Date Processed by STIC:		3	9	06	
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RAW SEQUENCE LISTINGPATENT APPLICATION: **US/10/526,768**DATE: 03/09/2006

TIME: 12:31:28

Input Set : A:\seq listing XII 847-05.ST251.txt

Output Set: N:\CRF4\03092006\J526768.raw

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3 <110> APPLICANT: Forschungsverbund Berlin e.V.
      5 <120> TITLE OF INVENTION: AKAP18delta a novel splicing variant of a protein kinase A
anchor
      6
              protein and the use of the same
      8 <130> FILE REFERENCE: XII 843-05
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/526,768
C--> 11 <141> CURRENT FILING DATE: 2005-03-07
     13 <150> PRIOR APPLICATION NUMBER: DE 102 44 072.7
     14 <151> PRIOR FILING DATE: 2002-09-06
     16 <150> PRIOR APPLICATION NUMBER: DE 103 06 085.5
     17 <151> PRIOR FILING DATE: 2003-02-07
     19 <160> NUMBER OF SEQ ID NOS: 2
     21 <170> SOFTWARE: PatentIn version 3.3
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 1062
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Homo sapiens
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     31 gaggaaggga cgggggacct ggagaccagc cctgtaggtt ctctggcaga cctgccgttt
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     33 gctgccgtag acattcaaga tgactgtgga ctccctgatg tacctcaagg aaatgtacct
                                                                              180
     35 caaggaaacc caaagagaag caaagaaaat agaggcgaca ggaatgatca cgtgaagaag
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     37 aggaagaagg ccaagaaaga ttatcaaccc aactatttcc tgtccattcc aatcaccaac
                                                                              300
     39 aaaaagatta cagctggaat taaagtcttg caaaattcga tactgagaca ggataatcga
                                                                              360
     41 ttgaccaaag ccatggtcgg cgacggctcc tttcacatca ccttgctagt gatgcagcta
                                                                              420
     43 ttaaacgaag atgaagtaaa cataggtacc gacgcgcttt tggaactgaa gccgttcgtt
                                                                              480
     45 gaggagatcc ttgaggggaa gcatctgact ttgcccttcc acgggattgg cactttccaa
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     47 ggtcaggttg gctttgtgaa gctggcagac ggagatcacg tcagtgccct cctggagata
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     49 gcagagactg caaaaaggac atttcaggaa aaaggcatcc tggctggaga aagcagaact
                                                                              660
     51 tttaagcctc acctgacctt tatgaagctg tccaaagcac caatgctctg gaagaaggga
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     53 gtgagaaaaa tagagcctgg attgtatgag caatttatcg accacagatt tggagaagaa
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     55 atactgtacc aaatagatct ctgctccatg ctgaagaaaa aacagagcaa tggttattac
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    57 cactgcgagt cttcgatcgt gatcggtgag aaggaccgaa aggagcctga ggatgctgaa
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    59 ctggtcaggc tcagtaagag gctggtggag aacgccgtgc tcaaggctgt ccagcagtac
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    61 ctagaagaga cacagaacaa aaagcagccg ggggagggga actccgtcaa agctgaggag
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     69 <213> ORGANISM: Homo sapiens
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     77 Leu Ser Arg Gly Glu Glu Gly Thr Gly Asp Leu Glu Thr Ser Pro Val
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78				20					25					30		
81 (Gly	Ser	Leu	Ala	Asp	Leu	Pro	Phe	Ala	Ala	Val	Asp	Ile	Gln	Asp	Asp
82	_		35		_			40					45			
85 (Cys	Gly	Leu	Pro	Asp	Val	Pro	Gln	Gly	Asn	Val	Pro	Gln	Gly	Asn	Pro
86	_	50					55					60				
89	Lys	Arg	Ser	Lys	Glu	Asn	Arg	Gly	Asp	Arg	Asn	Asp	His	Val	Lys	Lys
90	65					70					75					80
93 2	Arg	Lys	Lys	Ala	Lys	Lys	Asp	Tyr	Gln	Pro	Asn	Tyr	Phe	Leu	Ser	Ile
94					85					90					95	
97	Pro	Ile	Thr	Asn	Lys	Lys	Ile	Thr	Ala	Gly	Ile	Lys	Val	Leu	Gln	Asn
98				100					105					110		
101	Ser	Ile	. Let	ı Arg	, Glr	ı Asp	Asn	Arg	Let	Thr	Lys	: Ala	Met	. Val	. Gly	/ Asp
102			115	5				120)				125	5		
105	Gly	Ser	Phe	His	: Ile	Thr	Leu	Lei	ı Val	Met	Glr	Let	ı Leı	ı Asr	ı Glı	ı Asp
106		130)				135	;				140)			
109	Glu	Val	Asr	ıle	: Gly	Thr	Asp	Ala	Let	Let	ı Glu	Let	Lys	Pro	Phe	val
110	145					150)				155	;				160
113	Glu	Glu	Ile	e Lev	ı Glı	ı Gly	Lys	His	Lev	Thr	Leu	ı Pro	Phe	e His	Gl _y	/ Ile
114					165	5				170)				175	5
117	Gly	Thr	Phe	Glr	ı Gly	/ Gln	. Val	. Gly	/ Phe	· Val	. Lys	Let	ı Ala	a Asp	Gly	/ Asp
118				180					185					190		
121	His	Val	. Ser	Ala	Let	ı Leu	ເ Glບ	ιIle	e Ala	Glu	Thr	Ala	Lys	ar <u>c</u>	J Thi	Phe
122			195					200					205			
125	Gln		_	Gly	, Ile	e Leu		_	/ Glu	Ser	Arg			e Lys	Pro	His
126		210					215					220				
			Phe	Met	Lys			Lys	: Ala	Pro			ıTr	Lys	Lys	Gly
	225		_		-	230		_	_		235			_		240
	Val	Arg	Lys	; Ile			GLy	Leu	ı Tyr			Phe	: Ile	e Asp		Arg
134	_,	~ 7	~7	~7	245		_	~-		250		~	_		255	
	Pne	GIY	GIU			e Leu	Tyr	GII		_	ь тел	Cys	s ser			Lys
138	T	.		260					265					270		T1.
	ьys	гуѕ			ASI	і Сіу	туг	_		Cys	GIU	ser			val	. Ile
142	a 1		275		. 7		. al	280		7 ~~		. al.	285		7	. Ta
	GIY	290	_	ASP	AIG	ј гув	295) GIU	ASL) Ala	300		ı vaı	. Arg	Leu
146	Com					C1				Ton				~1-		Птт
	305	_	MIG	ιнеυ	ı val	. Glu 310		HIS	. val	Let	. шуя 315		. val	. G11.		Tyr 320
			G1.	. ሞኤ~	· @1 ~			T 120	, dl~	Dro			G1.	, 7.a-	CA*	Val
154	теп	GIU	GIU	. 1111	325		. шуы	, пус	, GII	330		GIL	. Gly	ASI.	335	
	Lare	λ 1 ⇒	G1v	(21)			Δτο	λον	വ			Cor	· Acr	λον		Arg
158	пys	ATO	GIU	340	_	Lop	Arg	, ASI.	345	_	, Gry	DCI	Lop	350		. Arg
	Lys			240	,				243					550	,	
101	шyэ															

VERIFICATION SUMMARY

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L:10~M:270~C: Current Application Number differs, Replaced Current Application Number L:11~M:271~C: Current Filing Date differs, Replaced Current Filing Date